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Genome Announcements

Draft genome sequence of a GES-5-producing *Serratia marcescens* isolated in southern Brazil

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ABSTRACT

Serratia marcescens is a Gram-negative rod intrinsically resistant to polymyxins and usually associated with wound, respiratory and urinary tract infections. The whole genome of the first GES-5-producing *S. marcescens* isolated from a Brazilian patient was sequenced using Ion Torrent PGM System. Besides bla_{GES-5}, we were able to identify genes encoding for other β-lactamases, for aminoglycoside modifying enzymes and for an efflux pump to tetracyclines.

Nowadays carbapenemase production is the main carbapenem resistance mechanism among *Enterobacteriaceae*.[1] The Guiana Extended-Spectrum (GES) β-lactamase family comprises several Ambler class A enzymes with distinguished β-lactam hydrolysis profiles. The original GES were classified as extended-spectrum β-lactamases (ESBL), but amino acid substitutions in the GES-type ESBLs enhanced their activity against carbapenems.[2] The GES-5 is the GES-carbapenemase which hydrolyses imipenem most efficiently.[3] Here we report the draft genome of the first GES-5-producing *Serratia marcescens* reported in Brazil.

As part of a surveillance study,[4] isolates with reduced susceptibility to carbapenems were submitted to Real Time (RT) High Resolution Melting (HRM) Multiplex PCR with specific primers for bla_{NDM}, bla_{KPC}, bla_{VIM}, bla_{GES}, $bla_{OXA-48-like}$ and bla_{IMP}.[5] One isolate, obtained from an ascitic fluid of a female patient in a tertiary hospital in Porto Alegre (Brazil) in October 2014, and identified as *S. marcescens* by the Vitek2 system, presented an amplicon with a Temperature of Melting (Tm) similar to the bla_{GES} positive control in the RT-PCR – 85.32 °C and 85.52 °C, respectively. Antimicrobial susceptibility was determined by Etest and the isolate presented high resistance levels to carbapenems (MIC > 32 mg/L) and polymyxins (MIC > 256 mg/L), but remained susceptible to fluoroquinolones and tigecycline.

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Whole genome sequencing (WGS) was performed using the Ion Torrent PGM™ system, with a 400-bp-read kit and a 316™ Chip. Library was previously obtained by enzymatic fragmentation. We obtained 997,155 reads with a mean read length of 232 bp. The reads were assembled in contigs using SPAdes.[6] The assembling revealed a 5,378,959 bp length genome, distributed in 208 contigs (≥500 bp), with a total GC content of 59%.

The contigs were annotated using the NCBI pipeline[7] and manually curated using Artemis,[8] when necessary. We also submitted the contigs to ResFinder Database.[9] Annotation revealed 3657 CDS, as well as 70 tRNA and 14 rRNA genes. As expected, we were able to identify the presence of bla_{GES-5} (locus tag AN414_25255) after annotation, as well as genes coding for other β-lactamases ($bla_{CTX-M-2}$ and bla_{OXA-2}, locus tags AN414_24540 and AN414_25310, respectively), and aminoglycoside modifying enzymes (*aac*(3)-IIa and *aac*(6′)-Ic, locus tags AN414_24600 and AN414_08220, respectively). We were also able to observe the presence of a gene coding for an efflux pump to tetracyclines (*tet*(41), locus tag AN414_07940). The location of the resistance determinants in the genome (chromosome or plasmid borne) was not determined. To the best of our knowledge, this is the first report of a GES-5-producing *S. marcescens* in Brazil. We also demonstrated that NGS platforms can be used as a valuable tool to evaluate resistance determinants among *Enterobacteriaceae*.

Accession number: This whole-genome shotgun project has been deposited at GenBank under the accession number LNZT00000000. The version described in this paper is in the first version, LNZT01000000. The BioProject ID is PRJNA294719.

Conflicts of interest

The authors declare no conflicts of interest.

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